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L1   ANSWER 1 OF 1  HCAPLUS  COPYRIGHT 2004 ACS on STN
AN   2002:539911  HCAPLUS
DN   137:90576
ED   Entered STN:  19 Jul 2002
TI   Stable isotope, site-specific mass tagging for protein identification
IN   Chen, Xian
PA   The Regents of the University of California, USA
SO   PCT Int. Appl., 38 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
IC   ICM  G01N
CC   9-5 (Biochemical Methods)
FAN.CNT 1
     PATENT NO.        KIND  DATE          APPLICATION NO.  DATE
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PI   WO 2002055989     A2    20020718      WO 2002-US538    20020111
     WO 2002055989     A3    20021128
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM,
             HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,
             LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO,
             RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN,
             YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH,
             CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR,
             BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
     US 2002146743     A1    20021010      US 2002-43965    20020111 <--
PRAI US 2001-261716P   P     20010112
AB   Proteolytic peptide mass mapping as measured by mass spectrometry provides
     an important method for the identification of proteins, which are usually
     identified by matching the measured and calculated m/z values of the
     proteolytic peptides.  A unique identification is, however, heavily
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dependent upon the mass accuracy and sequence coverage of the fragment ions generated by peptide ionization. The present invention describes a method for increasing the specificity, accuracy and efficiency of the assignments of particular proteolytic peptides and consequent protein identification, by the incorporation of selected amino acid residue(s) enriched with stable isotope(s) into the protein sequence without the need for ultrahigh instrumental accuracy. Selected amino acids(s) are labeled. With 13C/15N/2H and incorporated into proteins in a sequence-specific manner during cell culturing. Each of these labeled amino acids carries a defined mass change encoded in its monoisotopic distribution pattern. Through their characteristic patterns, the peptides with mass tag(s) can be readily distinguished from other peptides in mass spectra. The present method of identifying unique proteins can also be extended to protein complexes and will significantly increase data search specificity, efficiency and accuracy for protein identifications.

ST stable isotope mass tagging protein

IT Mass spectra
(Delayed-extraction; stable isotope, site-specific mass tagging for protein identification)

IT Mass spectra
(Postsource decay fragment ion; stable isotope, site-specific mass tagging for protein identification)

IT Peptides, analysis
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(UBL1; stable isotope, site-specific mass tagging for protein identification)

IT Proteins
RL: ANT (Analyte); ANST (Analytical study)
(complexes; stable isotope, site-specific mass tagging for protein identification)

IT Mass spectrometers
(electrospray-ionization; stable isotope, site-specific mass tagging for protein identification)

IT Gene
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(expression; stable isotope, site-specific mass tagging for protein identification)

IT Amino acids, uses
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(labeled; stable isotope, site-specific mass tagging for protein identification)

IT Gene
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(lesions; stable isotope, site-specific mass tagging for protein identification)

IT Time-of-flight mass spectrometers
(matrix-assisted laser desorption/ionization; stable isotope, site-specific mass tagging for protein identification)

IT Information systems
(searching; stable isotope, site-specific mass tagging for protein identification)

IT Cell
Composition
Digestion, chemical
Dilution
Escherichia coli
Ionization
Ions
Isotope indicators

Searched by Noble Jarrell 272-2556

Labels
Liquid chromatography
Mass
Mass spectra
Mass spectrometers
Mass spectrometry
Mathematical methods
Mixtures
Protein degradation
Protein sequences
Separation
(stable isotope, site-specific mass tagging for protein identification)

IT Peptides, analysis
Proteins
RL: ANT (Analyte); ANST (Analytical study)
(stable isotope, site-specific mass tagging for protein identification)

IT Proteome
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(stable isotope, site-specific mass tagging for protein identification)

IT Gel electrophoresis
(two-dimensional; stable isotope, site-specific mass tagging for protein identification)

IT 4896-75-7, Glycine-2,2-d2 7782-39-0, Hydrogen-2, uses 14390-96-6, Nitrogen-15, uses 14762-74-4, Carbon-13, uses 349086-43-7, L-Methionine-d3
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(stable isotope, site-specific mass tagging for protein identification)

IT 26112-89-0, Isopropylthiogalactoside
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(stable isotope, site-specific mass tagging for protein identification)

IT 9001-92-7, Protease 9002-07-7, Trypsin
RL: CAT (Catalyst use); USES (Uses)
(stable isotope, site-specific mass tagging for protein identification)

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